

[illegible]

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ACIDS ENCODING THE SAME

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<150> 60/068,017
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 gtagtacatg gtggataact tctactttta ggaggactac tctcttctga 200
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35 40 45
Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu
50 55 60
Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
65 70 75
Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
80 85 90
Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
95 100 105
Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
110 115 120
Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
125 130 135
Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
140 145 150
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155 160 165
Leu Asn Leu Pro Lys Ser Leu Ala Glu Leu Arg Ile His Glu Asn
170 175 180
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185 190 195
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Abstract The purpose of this study was to determine the effect of a 12-week training program on the heart rate (HR) and blood pressure (BP) of sedentary, middle-aged men. The subjects were divided into two groups: a control group and an exercise group. The control group consisted of 10 men who did not exercise, and the exercise group consisted of 10 men who exercised for 12 weeks. The HR and BP were measured at baseline and at the end of the 12-week period. The results showed that the exercise group had a significant decrease in HR and BP compared to the control group. The HR of the exercise group decreased from 72.5 ± 5.0 beats/min at baseline to 68.5 ± 4.0 beats/min at the end of the 12-week period. The BP of the exercise group decreased from 120/80 mmHg at baseline to 110/70 mmHg at the end of the 12-week period. The control group showed no significant change in HR and BP. The results of this study suggest that a 12-week training program can effectively reduce HR and BP in sedentary, middle-aged men.

[illegible]

<211> 954

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35 40 45

Arg Gly Ala Ala Gly Cys Thr Phe Gly Gly Lys Val Tyr Ala Leu
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Asp Glu Thr Trp His Pro Asp Leu Gly Gln Pro Phe Gly Val Met
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35 40 45

Gly Pro Cys Ala Ala Gln Pro Cys Arg Asn Gly Gly Val Cys Thr
50 55 60

Ser Arg Pro Glu Pro Asp Pro Gln His Pro Ala Pro Ala Gly Glu
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Pro Gly Tyr Ser Cys Thr Cys Pro Ala Gly Ile Ser Gly Ala Asn
80 85 90

Cys Gln Leu Val Ala Asp Pro Cys Ala Ser Asn Pro Cys His His
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16

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Leu	Thr	Asn	Met	635	Pro	Arg	His	Ser	640	Tyr	Ile	Ile	Ile	Gly	Ala
Leu	Cys	Val	Ala	650	Phe	Ile	Leu	Met	655	Ile	Ile	Leu	Ile	Val	Gly
Ile	Cys	Arg	Ile	665	Ser	Arg	Ile	Glu	670	Gln	Gly	Ser	Ser	Arg	Pro
Ala	Tyr	Glu	Glu	680	Phe	Tyr	Asn	Cys	685	Ser	Ile	Asp	Ser	Glu	Phe
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695

700

705

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aagatgggag caatttcacc tgtgtttgcc ttctgggtta tactggagag 450

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<212> PRT

<213> Homo Sapien

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Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Leu	Val	Leu	Arg	Gln		35	40	45	
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Ala	Gln	Phe	Trp	Ser	Ala	Tyr	Val	Pro	Cys	Gln	Thr	Gln	Asp	Arg		80	85	90	
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Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	Lys		110	115	120	
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Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Gly	Trp	Ser	Glu	Glu	320	325	330
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg	335	340	345
Gln	Val	Glu	Lys	Val	Gln	Glu	Glu	Asn	Lys	Trp	Gln	Ser	Pro	Leu	350	355	360
Glu	Asp	Lys	Phe	Pro	Asp	Glu	Gln	Leu	Ser	Ser	Ser	Cys	His	Ser	365	370	375
Asp	Leu	Ser	Arg	Leu	Arg	Gln	Arg	Gln	Ser	Leu	Thr	Ser	Gly	Gln	380	385	390
Glu	Leu	Thr	Glu	Ile	Pro	Ile	His	Trp	Thr	Ala	Lys	Leu	Pro	Ala	395	400	405
Lys	Trp	Ser	Val	Ser	Glu	Ser	Ser	Pro	His	Met	Ala	Pro	Val	Leu	410	415	420
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caatagcctc tccatcttac gtaccttcta catgctggga gtgcgctacc 550
tgacgctcac ccacacctgc aacacaccct gggcagagag ctccgctaag 600
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gccccttggg ggacaagttc ccggatgagc agctgagcag ttctgccac 1200
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cagtctcaga gtctctcccc caccctgaca aaactcacac atgcccaccg 1350
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aaaacccaag gacacc 1416

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<210> 30
<211> 446
<212> PRT
<213> Homo Sapien
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09443730-033001

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	65	70		75	
Ala Gln Phe Trp	Ser Ala Tyr Val Pro	Cys Gln Thr Gln Asp Arg			
	80	85		90	
Asp Ala Leu Arg	Leu Thr Leu Glu Gln	Ile Asp Leu Ile Arg Arg			
	95	100		105	
Met Cys Ala Ser	Tyr Ser Glu Leu Glu	Leu Val Thr Ser Ala Lys			
	110	115		120	
Ala Leu Asn Asp	Thr Gln Lys Leu Ala	Cys Leu Ile Gly Val Glu			
	125	130		135	
Gly Gly His Ser	Leu Asp Asn Ser Leu	Ser Ile Leu Arg Thr Phe			
	140	145		150	
Tyr Met Leu Gly	Val Arg Tyr Leu Thr	Leu Thr His Thr Cys Asn			
	155	160		165	
Thr Pro Trp Ala	Glu Ser Ser Ala Lys	Gly Val His Ser Phe Tyr			
	170	175		180	
Asn Asn Ile Ser	Gly Leu Thr Asp Phe	Gly Glu Lys Val Val Ala			
	185	190		195	
Glu Met Asn Arg	Leu Gly Met Met Val	Asp Leu Ser His Val Ser			
	200	205		210	
Asp Ala Val Ala	Arg Arg Ala Leu Glu	Val Ser Gln Ala Pro Val			
	215	220		225	
Ile Phe Ser His	Ser Ala Ala Arg Gly	Val Cys Asn Ser Ala Arg			
	230	235		240	
Asn Val Pro Asp	Asp Ile Leu Gln Leu	Leu Lys Lys Asn Gly Gly			
	245	250		255	
Val Val Met Val	Ser Leu Ser Met Gly	Val Ile Gln Cys Asn Pro			
	260	265		270	
Ser Ala Asn Val	Ser Thr Val Ala Asp	His Phe Asp His Ile Lys			
	275	280		285	
Ala Val Ile Gly	Ser Lys Phe Ile Gly	Ile Gly Gly Asp Tyr Asp			
	290	295		300	
Gly Ala Gly Lys	Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr			
	305	310		315	
Pro Val Leu Ile	Glu Glu Leu Leu Ser	Arg Gly Trp Ser Glu Glu			
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Glu Leu Gln Gly	Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg			
	335	340		345	

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atccgcgcgg cggccgcgcg cgttgctgcc cctgctgctg ctgctctgcy 200
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agtgcacgga gaccaccag gagccaccgc cgagggcctc tactggacct 350
tcaacgggcy ccgcctgccc cctgagctct cccgtgtact caacgcctcc 400
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gcctctatgt tggcctgccc ccagagaaac ccgtcaacat cagctgctgg 550
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ggagaccttc ctccacacca actactccct caagtacaag cttagggtgg 650
atggccagga caacacatgt gaggagtacc acacagtggg gcccactcc 700
tgccacatcc ccaaggacct ggctctcttt acgccctatg agatctgggt 750
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[illegible]

<211> 422

<213> Homo Sapien

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1 5 10 15

Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

28

094330-033001

Ser	Val	His	Gly	Asp	Pro	Pro	Gly	Ala	Thr	Ala	Glu	Gly	Leu	Tyr	65	70	75
Trp	Thr	Leu	Asn	Gly	Arg	Arg	Leu	Pro	Pro	Glu	Leu	Ser	Arg	Val	80	85	90
Leu	Asn	Ala	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly	95	100	105
Ser	Arg	Gln	Arg	Ser	Gly	Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp	110	115	120
Gly	Ser	Ile	Leu	Ala	Gly	Ser	Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro	125	130	135
Glu	Lys	Pro	Val	Asn	Ile	Ser	Cys	Trp	Ser	Lys	Asn	Met	Lys	Asp	140	145	150
Leu	Thr	Cys	Arg	Trp	Thr	Pro	Gly	Ala	His	Gly	Glu	Thr	Phe	Leu	155	160	165
His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr	Lys	Leu	Arg	Trp	Tyr	Gly	Gln	170	175	180
Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	Thr	Val	Gly	Pro	His	Ser	Cys	185	190	195
His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr	Pro	Tyr	Glu	Ile	Trp	200	205	210
Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg	Ser	Asp	Val	Leu	215	220	225
Thr	Leu	Asp	Ile	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro	Pro	Pro	Asp	230	235	240
Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	Leu	Ser	Val	245	250	255
Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln	Ala	260	265	270
Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys	275	280	285
Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly	290	295	300
Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro	305	310	315
Phe	Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp	320	325	330
Ser	His	Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly	335	340	345
Pro	Gly	Gly	Gly	Ala	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser			

350	355	360
Gly Pro Val Arg Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys		
365	370	375
Lys His Ala Tyr Cys Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln		
380	385	390
Trp Arg Ala Trp Met Gln Lys Ser His Lys Thr Arg Asn Gln Asp		
395	400	405
Glu Gly Ile Leu Pro Ser Gly Arg Arg Gly Thr Ala Arg Gly Pro		
410	415	420

Ala Arg

<210> 33
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 33
 cccgccccgac gtgcacgtga gcc 23

<210> 34
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 34
 tgagccagcc caggaactgc ttg 23

<210> 35
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 35
 caagtgcgct gcaaccctt tggcatctat ggctccaaga aagccgggat 50

<210> 36
 <211> 1771
 <212> DNA
 <213> Homo Sapien

<400> 36
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 ctccctagag tccttcgtga agctttttat tcctaagagg agaaaatcag 200
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 tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg 350
 gtgccaaggt tcataccttt gtggtagact gcagcaaccg agaagatatt 400
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 aacattggaa aggatccttc ctgagcggtt cctggcagtt ttaaaacgaa 950
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gccactctgt ttctgagag atacctcaca ttccaatgcc aaacatttct 1550
gcacagggaa gctagagggtg gatacacgtg ttgcaagtat aaaagcatca 1600
ctgggattta aggagaattg agagaatgta cccacaaatg gcagcaataa 1650
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<210> 37
<211> 300
<212> PRT
<213> Homo Sapien

<400> 37
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Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
35 40 45
His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys
50 55 60
Ser Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu
65 70 75
Thr Ala Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe
80 85 90
Val Val Asp Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys
95 100 105
Lys Val Lys Ala Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn
110 115 120
Ala Gly Val Val Tyr Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro
125 130 135
Gln Ile Glu Lys Thr Phe Glu Val Asn Val Leu Ala His Phe Trp
140 145 150
Thr Thr Lys Ala Phe Leu Pro Ala Met Thr Lys Asn Asn His Gly
155 160 165
His Ile Val Thr Val Ala Ser Ala Ala Gly His Val Ser Val Pro
170 175 180
Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe
185 190 195
His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile Thr Gly

200	205	210
Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly Phe		
215	220	225
Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu		
230	235	240
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys		
245	250	255
Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu		
260	265	270
Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile		
275	280	285
Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln		
290	295	300

<210> 38

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 38

ggtgaaggca gaaattggag atg 23

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 39

atcccatgca tcagcctgtt tacc 24

<210> 40

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

gctgggtgtag tctatacatc agatttggtt gctacacaag atcctcag 48

<210> 41

<211> 1377

<212> DNA

<213> Homo Sapien



<400> 41

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gaaccaggac tggggtgacg gcagggcagg gggcgcttg ccggggagaa 100
gcgcgggggc tggagcacca ccaactggag ggtccggagt agcgagcgcc 150
ccgaaggagg ccatcgggga gccgggaggg gggactgca gaggaccccg 200
gcgtccgggc tcccggtgcc agcgctatga ggccactcct cgtcctgctg 250
ctcctggggc tggcgccgg ctgccccca ctggacgaca acaagatccc 300
cagcctctgc ccggggcacc ccggccttcc aggcacgccg ggccaccatg 350
gcagccaggg cttgccgggc cgcgatggcc gcgacggccg cgacggcgcg 400
cccggggctc cgggagagaa aggcgagggc gggaggccgg gactgccggg 450
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cgaccgcgtg ctggtgaacg agcagggaca ttacgacgcc gtcaccggca 650
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gtctaccggg ccagcctgca gtttgatctg gtgaagaatg gcgaatccat 750
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aaaaaaaaa aaaaaaaaaa aaaaaaa 1377

<210> 42

<211> 243
 <212> PRT
 <213> Homo Sapien

<400> 42

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Ser	Pro	Pro	Leu	Asp	Asp	Asn	Lys	Ile	Pro	Ser	Leu	Cys	Pro	Gly	20	25	30	
His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly	35	40	45	
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro	Gly	50	55	60	
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro	Gly	65	70	75	
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala	Gly	80	85	90	
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser	Ala	95	100	105	
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser	Asp	110	115	120	
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly	His	125	130	135	
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly	Val	140	145	150	
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu	Gln	155	160	165	
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe	Gln	170	175	180	
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly	Ala	185	190	195	
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val	Gly	200	205	210	
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp	Ser	215	220	225	
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser	Pro	230	235	240	
Val	Phe	Ala																

<210> 43
 <211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 43
 tacaggccca gtcaggacca gggg 24

 <210> 44
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 44
 agccagcctc gctctcgg 18

 <210> 45
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 45
 gtctgcatc aggtctgg 18

 <210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 46
 gaaagaggca atggattcgc 20

 <210> 47
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 47
 gacttacact tgccagcaca gcac 24

 <210> 48
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49

<211> 1876

<212> DNA

<213> Homo Sapien

<400> 49

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atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100
acctgacggg cccaacagac ccatgctgca tccagagacc tcccctggcc 150
gggggcatct cctggctgtg ctcttgccc tccttggcac cacctgggca 200
gaggtgtggc caccagct gcaggagcag gctccgatgg ccggagccct 250
gaacaggaag gagagtttct tgtcctctc cctgcacaac cgctgcgca 300
gctgggtcca gcccctgcg gctgacatgc ggaggctgga ctggagtgc 350
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cccgagcctg gcacccggcc tgtggcgcac cctgcaagtg ggctggaaca 450
tgcagctgtc gcccgcgggc ttggcgctct ttgttgaagt ggtcagccta 500
tggtttgcag aggggcagcg gtacagccac gcggcaggag agtgtgctcg 550
caacgccacc tgcacccact acacgcagct cgtgtggggc acctcaagcc 600
agctgggctg tgggcggcac ctgtgctctg caggccagac agcgatagaa 650
gcctttgtct gtgcctactc ccccgaggc aactgggagg tcaacgggaa 700
gacaatcatc cccataaga aggggtgcctg gtgttcgctc tgcacagcca 750
gtgtctcagg ctgcttcaaa gcctgggacc atgcaggggg gctctgtgag 800
gtccccagga atccttgtcg catgagctgc cagaacctg gacgtctcaa 850
catcagcacc tgccactgcc actgtcccc tggctacacg ggcagatact 900
gccaagtgcg gtgcagcctg cagtgtgtgc acggccgggt ccgggaggag 950
gagtgtcgt gcgtctgtga catcggtac gggggagccc agtgtgccac 1000
caaggtgcat ttcccttcc acacctgtga cctgaggatc gacggagact 1050
gcttcatggt gtcttcagag gcagacacct attacagagc caggatgaaa 1100
tgtcagagga aaggcggggt gctggcccag atcaagagcc agaaagtgc 1150

[illegible]

<211> 455

<212> PRT

<213> Hom

Met Leu His Pro Glu Thr Ser Pro Gly Arg Gly His Leu Leu Ala
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Val Leu Leu Ala Leu Leu Gly Thr Thr Trp Ala Glu Val Trp Pro
20 25 30

Pro Gln Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg
35 40 45

Lys Glu Ser Phe Leu Leu Leu Ser Leu His Asn Arg Leu Arg Ser
50 55 60

Trp Val Gln Pro Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser
65 70 75

Asp Ser Leu Ala Gln Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly
80 85 90

Ile Pro Thr Pro Ser Leu Ala Ser Gly Leu Trp Arg Thr Leu Gln
95 100 105

Val Gly Trp Asn Met Gln Leu Leu Pro Ala Gly Leu Ala Ser Phe

				110					115					120
Val	Glu	Val	Val	Ser 125	Leu	Trp	Phe	Ala	Glu 130	Gly	Gln	Arg	Tyr	Ser 135
His	Ala	Ala	Gly	Glu 140	Cys	Ala	Arg	Asn	Ala 145	Thr	Cys	Thr	His	Tyr 150
Thr	Gln	Leu	Val	Trp 155	Ala	Thr	Ser	Ser	Gln 160	Leu	Gly	Cys	Gly	Arg 165
His	Leu	Cys	Ser	Ala 170	Gly	Gln	Thr	Ala	Ile 175	Glu	Ala	Phe	Val	Cys 180
Ala	Tyr	Ser	Pro	Gly 185	Gly	Asn	Trp	Glu	Val 190	Asn	Gly	Lys	Thr	Ile 195
Ile	Pro	Tyr	Lys	Lys 200	Gly	Ala	Trp	Cys	Ser 205	Leu	Cys	Thr	Ala	Ser 210
Val	Ser	Gly	Cys	Phe 215	Lys	Ala	Trp	Asp	His 220	Ala	Gly	Gly	Leu	Cys 225
Glu	Val	Pro	Arg	Asn 230	Pro	Cys	Arg	Met	Ser 235	Cys	Gln	Asn	His	Gly 240
Arg	Leu	Asn	Ile	Ser 245	Thr	Cys	His	Cys	His 250	Cys	Pro	Pro	Gly	Tyr 255
Thr	Gly	Arg	Tyr	Cys 260	Gln	Val	Arg	Cys	Ser 265	Leu	Gln	Cys	Val	His 270
Gly	Arg	Phe	Arg	Glu 275	Glu	Glu	Cys	Ser	Cys 280	Val	Cys	Asp	Ile	Gly 285
Tyr	Gly	Gly	Ala	Gln 290	Cys	Ala	Thr	Lys	Val 295	His	Phe	Pro	Phe	His 300
Thr	Cys	Asp	Leu	Arg 305	Ile	Asp	Gly	Asp	Cys 310	Phe	Met	Val	Ser	Ser 315
Glu	Ala	Asp	Thr	Tyr 320	Tyr	Arg	Ala	Arg	Met 325	Lys	Cys	Gln	Arg	Lys 330
Gly	Gly	Val	Leu	Ala 335	Gln	Ile	Lys	Ser	Gln 340	Lys	Val	Gln	Asp	Ile 345
Leu	Ala	Phe	Tyr	Leu 350	Gly	Arg	Leu	Glu	Thr 355	Thr	Asn	Glu	Val	Thr 360
Asp	Ser	Asp	Phe	Glu 365	Thr	Arg	Asn	Phe	Trp 370	Ile	Gly	Leu	Thr	Tyr 375
Lys	Thr	Ala	Lys	Asp 380	Ser	Phe	Arg	Trp	Ala 385	Thr	Gly	Glu	His	Gln 390
Ala	Phe	Thr	Ser	Phe 395	Ala	Phe	Gly	Gln	Pro 400	Asp	Asn	His	Gly	Leu 405

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
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<213> Homo Sapien

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Asp	Lys	Ala	Ala	Phe 155	Phe	Leu	Ser	Tyr	Glu 160	Glu	Leu	Leu	Gln	Arg 165
Arg	Leu	Gly	Lys	Tyr 170	Glu	His	Ser	Ile	Ser 175	Val	Arg	Pro	Gln	Gln 180
Leu	Ser	Gly	Arg	Leu 185	Ser	Val	Asp	Val	Asn 190	Ile	Leu	Glu	Ser	Ala 195
Gly	Ile	Ala	Ser	Leu 200	Glu	Val	Leu	Pro	Leu 205	His	Asn	Ser	Arg	Gln 210
Arg	Gly	Ser	Gly	Arg 215	Gly	Glu	Asp	Asp	Ser 220	Gly	Pro	Pro	Pro	Ser 225
Thr	Val	Ile	Asn	Gln 230	Asn	Glu	Thr	Phe	Ala 235	Asn	Ile	Ile	Phe	Lys 240
Pro	Thr	Val	Val	Gln 245	Gln	Ala	Arg	Ile	Ala 250	Gln	Asn	Gly	Ile	Leu 255
Gly	Asp	Phe	Ile	Ile 260	Arg	Tyr	Asp	Val	Asn 265	Arg	Glu	Gln	Ser	Ile 270
Gly	Asp	Ile	Gln	Val 275	Leu	Asn	Gly	Tyr	Phe 280	Val	His	Tyr	Phe	Ala 285
Pro	Lys	Asp	Leu	Pro 290	Pro	Leu	Pro	Lys	Asn 295	Val	Val	Phe	Val	Leu 300
Asp	Ser	Ser	Ala	Ser 305	Met	Val	Gly	Thr	Lys 310	Leu	Arg	Gln	Thr	Lys 315
Asp	Ala	Leu	Phe	Thr 320	Ile	Leu	His	Asp	Leu 325	Arg	Pro	Gln	Asp	Arg 330
Phe	Ser	Ile	Ile	Gly 335	Phe	Ser	Asn	Arg	Ile 340	Lys	Val	Trp	Lys	Asp 345
His	Leu	Ile	Ser	Val 350	Thr	Pro	Asp	Ser	Ile 355	Arg	Asp	Gly	Lys	Val 360
Tyr	Ile	His	His	Met 365	Ser	Pro	Thr	Gly	Gly 370	Thr	Asp	Ile	Asn	Gly 375
Ala	Leu	Gln	Arg	Ala 380	Ile	Arg	Leu	Leu	Asn 385	Lys	Tyr	Val	Ala	His 390
Ser	Gly	Ile	Gly	Asp 395	Arg	Ser	Val	Ser	Leu 400	Ile	Val	Phe	Leu	Thr 405
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<210> 58
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<220>
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<400> 58
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<211> 440

<212> PRT

<213> Homo Sapien

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Phe	Thr	Lys	Asp	Val	Thr	Val	Ile	Glu	Gly	Glu	Val	Ala	Thr	Ile	
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Ser	Cys	Gln	Val	Asn	Lys	Ser	Asp	Asp	Ser	Val	Ile	Gln	Leu	Leu	
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Asn	Pro	Asn	Arg	Gln	Thr	Ile	Tyr	Phe	Arg	Asp	Phe	Arg	Pro	Leu	
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Lys	Asp	Ser	Arg	Phe	Gln	Leu	Leu	Asn	Phe	Ser	Ser	Ser	Glu	Leu	
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Lys	Val	Ser	Leu	Thr	Asn	Val	Ser	Ile	Ser	Asp	Glu	Gly	Arg	Tyr	
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Phe	Cys	Gln	Leu	Tyr	Thr	Asp	Pro	Pro	Gln	Glu	Ser	Tyr	Thr	Thr	
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Ile	Thr	Val	Leu	Val	Pro	Pro	Arg	Asn	Leu	Met	Ile	Asp	Ile	Gln	
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Lys	Asp	Thr	Ala	Val	Glu	Gly	Glu	Glu	Ile	Glu	Val	Asn	Cys	Thr	
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Ala	Met	Ala	Ser	Lys	Pro	Ala	Thr	Thr	Ile	Arg	Trp	Phe	Lys	Gly	
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Asn	Thr	Glu	Leu	Lys	Gly	Lys	Ser	Glu	Val	Glu	Glu	Trp	Ser	Asp	
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Thr	Gly	Asn	Leu	Gln	Thr	Gln	Arg	Tyr	Leu	Glu	Val	Gln	Tyr	Lys	
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Pro	Gln	Val	His	Ile	Gln	Met	Thr	Tyr	Pro	Leu	Gln	Gly	Leu	Thr	
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Arg	Glu	Gly	Asp	Ala	Leu	Glu	Leu	Thr	Cys	Glu	Ala	Ile	Gly	Lys	
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Pro	Gln	Pro	Val	Met	Val	Thr	Trp	Val	Arg	Val	Asp	Asp	Glu	Met	
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Pro	Gln	His	Ala	Val	Leu	Ser	Gly	Pro	Asn	Leu	Phe	Ile	Asn	Asn	
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Leu	Asn	Lys	Thr	Asp	Asn	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ser	Asn	

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335	340	345
Thr Thr Thr Thr Thr Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg		
350	355	360
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365	370	375
Gly Gly Val Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu		
380	385	390
Ile Ile Leu Gly Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe		
395	400	405
Thr His Glu Ala Lys Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr		
410	415	420
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Lys Glu Tyr Phe Ile		
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atcatcacag attcccagc 20

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ttcaatctcc tcaccttcca ccgc 24

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35 40 45
Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe
50 55 60
Glu Asn Gly Ile Thr Met Leu Asp Ala Ser Ser Phe Ala Gly Leu
65 70 75
Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser
80 85 90
Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu Ser His Asn Ser
95 100 105
Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu

				110					115					120
Ala	Leu	Arg	Leu	Ala	Gly	Leu	Gly	Leu	Gln	Gln	Leu	Asp	Glu	Gly
				125					130					135
Leu	Phe	Ser	Arg	Leu	Arg	Asn	Leu	His	Asp	Leu	Asp	Val	Ser	Asp
				140					145					150
Asn	Gln	Leu	Glu	Arg	Val	Pro	Pro	Val	Ile	Arg	Gly	Leu	Arg	Gly
				155					160					165
Leu	Thr	Arg	Leu	Arg	Leu	Ala	Gly	Asn	Thr	Arg	Ile	Ala	Gln	Leu
				170					175					180
Arg	Pro	Glu	Asp	Leu	Ala	Gly	Leu	Ala	Ala	Leu	Gln	Glu	Leu	Asp
				185					190					195
Val	Ser	Asn	Leu	Ser	Leu	Gln	Ala	Leu	Pro	Gly	Asp	Leu	Ser	Gly
				200					205					210
Leu	Phe	Pro	Arg	Leu	Arg	Leu	Leu	Ala	Ala	Ala	Arg	Asn	Pro	Phe
				215					220					225
Asn	Cys	Val	Cys	Pro	Leu	Ser	Trp	Phe	Gly	Pro	Trp	Val	Arg	Glu
				230					235					240
Ser	His	Val	Thr	Leu	Ala	Ser	Pro	Glu	Glu	Thr	Arg	Cys	His	Phe
				245					250					255
Pro	Pro	Lys	Asn	Ala	Gly	Arg	Leu	Leu	Leu	Glu	Leu	Asp	Tyr	Ala
				260					265					270
Asp	Phe	Gly	Cys	Pro	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Val	Pro	Thr
				275					280					285
Thr	Arg	Pro	Val	Val	Arg	Glu	Pro	Thr	Ala	Leu	Ser	Ser	Ser	Leu
				290					295					300
Ala	Pro	Thr	Trp	Leu	Ser	Pro	Thr	Ala	Pro	Ala	Thr	Glu	Ala	Pro
				305					310					315
Ser	Pro	Pro	Ser	Thr	Ala	Pro	Pro	Thr	Val	Gly	Pro	Val	Pro	Gln
				320					325					330
Pro	Gln	Asp	Cys	Pro	Pro	Ser	Thr	Cys	Leu	Asn	Gly	Gly	Thr	Cys
				335					340					345
His	Leu	Gly	Thr	Arg	His	His	Leu	Ala	Cys	Leu	Cys	Pro	Glu	Gly
				350					355					360
Phe	Thr	Gly	Leu	Tyr	Cys	Glu	Ser	Gln	Met	Gly	Gln	Gly	Thr	Arg
				365					370					375
Pro	Ser	Pro	Thr	Pro	Val	Thr	Pro	Arg	Pro	Pro	Arg	Ser	Leu	Thr
				380					385					390
Leu	Gly	Ile	Glu	Pro	Val	Ser	Pro	Thr	Ser	Leu	Arg	Val	Gly	Leu
				395					400					405

Gln Arg Tyr Leu	Gln Gly Ser Ser Val	Gln Leu Arg Ser Leu Arg
410		420
Leu Thr Tyr Arg	Asn Leu Ser Gly Pro	Asp Lys Arg Leu Val Thr
425		435
Leu Arg Leu Pro	Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu	
440		450
Arg Pro Asn Ala	Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro	
455		465
Gly Arg Val Pro	Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr	
470		480
Pro Pro Ala Val	His Ser Asn His Ala Pro Val Thr Gln Ala Arg	
485		495
Glu Gly Asn Leu	Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val	
500		510
Leu Leu Ala Ala	Leu Ala Ala Val Gly Ala Ala Tyr Cys Val Arg	
515		525
Arg Gly Arg Ala	Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val	
530		540
Gly Pro Gly Ala	Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro	
545		555
Leu Glu Pro Gly	Pro Lys Ala Thr Glu Gly Gly Gly Glu Ala Leu	
560		570
Pro Ser Gly Ser	Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly	
575		585
Pro Gly Leu Gln	Ser Pro Leu His Ala Lys Pro Tyr Ile	
590		595

<210> 70

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ccctccactg cccaccgac tg 22

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71
cggttctggg gacgttaggg ctcg 24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
ctgcccacccg tccacctgcc tcaat 25

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 73
aggactgcc accgtccacc tgcctcaatg ggggcacatg ccacc 45

<210> 74
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 74
acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75
<211> 1077
<212> DNA
<213> Homo Sapien

<400> 75
ggcactagga caaccttctt cccttctgca ccactgcccg taccottacc 50
cgccccgcca cctccttget accccactct tgaaaccaca gctgttggca 100
gggtccccag ctcatgccag cctcatctcc tttcttgcta gccccaaaag 150
ggcctccagg caacatgggg ggcccagtc gagagccggc actctcagtt 200
gccctctggt tgagttgggg ggcagctctg ggggccgtgg cttgtgccat 250
ggctctgctg acccaacaaa cagagctgca gagcctcagg agagaggtga 300
gccggctgca ggggacagga ggcccctccc agaatgggga agggatatccc 350
tggcagagtc tcccggagca gagttccgat gccctggaag cctgggagaa 400

tggggagaga tcccggaaaa ggagagcagt gctcacccaa aaacagaaga 450
 agcagcactc tgtcctgcac ctggttccca ttaacgccac ctccaaggat 500
 gactccgatg tgacagaggt gatgtggcaa ccagctctta ggcgtgggag 550
 aggcctacag gccaaggat atggtgtccg aatccaggat gctggagttt 600
 atctgctgta tagccaggtc ctgtttcaag acgtgacttt caccatgggt 650
 caggtggtgt ctcgagaagg ccaaggaagg caggagactc tattccgatg 700
 tataagaagt atgccctccc acccggaccg ggcctacaac agctgctata 750
 gcgcaggtgt cttccattta caccaagggg atattctgag tgtcataatt 800
 ccccgggcaa gggcgaaact taacctctct ccacatggaa ccttctctggg 850
 gtttgtgaaa ctgtgattgt gttataaaaa gtggctccca gcttggaaga 900
 ccagggtggg tacatactgg agacagccaa gagctgagta tataaaggag 950
 agggaatgtg caggaacaga ggcattcttc tgggtttggc tcccgttcc 1000
 tcacttttcc cttttcattc ccaccccta gactttgatt ttacggatat 1050
 cttgcttctg ttcccatgg agctccg 1077

<210> 76
 <211> 250
 <212> PRT
 <213> Homo Sapien

<400> 76
 Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro
 1 5 10 15
 Gly Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala
 20 25 30
 Leu Trp Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala
 35 40 45
 Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg
 50 55 60
 Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly
 65 70 75
 Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala
 80 85 90
 Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala
 95 100 105
 Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His Leu
 110 115 120

Val	Pro	Ile	Asn	Ala	Thr	Ser	Lys	Asp	Asp	Ser	Asp	Val	Thr	Glu
			125						130					135
Val	Met	Trp	Gln	Pro	Ala	Leu	Arg	Arg	Gly	Arg	Gly	Leu	Gln	Ala
			140						145					150
Gln	Gly	Tyr	Gly	Val	Arg	Ile	Gln	Asp	Ala	Gly	Val	Tyr	Leu	Leu
			155						160					165
Tyr	Ser	Gln	Val	Leu	Phe	Gln	Asp	Val	Thr	Phe	Thr	Met	Gly	Gln
			170						175					180
Val	Val	Ser	Arg	Glu	Gly	Gln	Gly	Arg	Gln	Glu	Thr	Leu	Phe	Arg
			185						190					195
Cys	Ile	Arg	Ser	Met	Pro	Ser	His	Pro	Asp	Arg	Ala	Tyr	Asn	Ser
			200						205					210
Cys	Tyr	Ser	Ala	Gly	Val	Phe	His	Leu	His	Gln	Gly	Asp	Ile	Leu
			215						220					225
Ser	Val	Ile	Ile	Pro	Arg	Ala	Arg	Ala	Lys	Leu	Asn	Leu	Ser	Pro
			230						235					240
His	Gly	Thr	Phe	Leu	Gly	Phe	Val	Lys	Leu					
			245						250					

<210> 77
 <211> 2849
 <212> DNA
 <213> Homo Sapien

<400> 77
 cactttctcc ctctcttctt ttacttttcca gaaaccgcgc ttccgcttct 50
 ggctgcagag acctcggaga ccgcgccggg gagacggagg tgctgtgggt 100
 gggggggacc tgtggctgct cgtaccgccc cccaccctcc tcttctgcac 150
 tgccgtcttc cggaagacct tttcccttgc tctgttttct tcaccgagtc 200
 tgtgcatcgc cccggacctg gccgggagga ggcttggccg gcgggagatg 250
 ctctaggggc ggccggggag gagcgccgg cgggacggag ggcccggcag 300
 gaagatgggc tcccgaggac agggactctt gctggcgtag tgccgtctcc 350
 ttgcctttgc ctctggcctg gtctgagtc gtgtgcccc tgtccagggg 400
 gaacagcagg agtgggagg gactgaggag ctgccgtcgc ctccggacca 450
 tgccgagagg gctgaagaac aacatgaaaa atacaggccc agtcaggacc 500
 aggggctccc tgcttcccg tgcttgcgct gctgtgaccc cggtagctcc 550
 atgtaccgg cgaccgccgt gcccagatc aacatcacta tcttgaaagg 600
 ggagaagggt gaccgcggag atcgaggcct ccaagggaat tatggcaaaa 650

caggctcagc	aggggcccagg	ggccacactg	gacccaaagg	gcagaagggc	700
tccatggggg	cccctgggga	gcggtgcaag	agccactacg	ccgccttttc	750
ggtggggccgg	aagaagccca	tgcacagcaa	ccactactac	cagacggtga	800
tcttcgacac	ggagttcgtg	aacctctacg	accacttcaa	catgttcacc	850
ggcaagttct	actgctacgt	gcccggcctc	tactttctca	gcctcaacgt	900
gcacacctgg	aaccagaagg	agacctacct	gcacatcatg	aagaacgagg	950
aggaggtggt	gatcttgttc	gcgcagggtg	gcgaccgcag	catcatgcaa	1000
agccagagcc	tgatgctgga	gctgcgagag	caggaccagg	tgtgggtacg	1050
cctctacaag	ggcgaacgtg	agaacgccat	cttcagcgag	gagctggaca	1100
cctacatcac	cttcagtggc	tacctggtca	agcacgccac	cgagccctag	1150
ctggccggcc	acctcctttc	ctctcgccac	cttcacccc	tgcgctgtgc	1200
tgaccccacc	gcctcttccc	cgatccctgg	actccgactc	cctggctttg	1250
gcattcagtg	agacgccctg	cacacacaga	aagccaaagc	gatcgggtgt	1300
cccagatccc	gcagcctctg	gagagagctg	acggcagatg	aaatcaccag	1350
ggcggggcac	ccgcgagaac	cctctgggac	cttcgcgggc	cctctctgca	1400
cacatcctca	agtgaccccg	cacggcgaga	cgcggggtgg	ggcagggcgt	1450
cccaggggtg	ggcacccggg	ctccagtcct	tggaaataat	taggcaaatt	1500
ctaaaggctc	caaaaggagc	aaagtaaacc	gtggaggaca	aagaaaaggg	1550
ttgttatttt	tgtctttcca	gccagcctgc	tggctcccaa	gagagaggcc	1600
ttttcagttg	agactctgct	taagagaaga	tccaaagtta	aagctctggg	1650
gtcaggggag	gggccggggg	caggaaacta	cctctggctt	aattctttta	1700
agccacgtag	gaactttctt	gagggatagg	tggaccctga	catccctgtg	1750
gccttgccca	agggctctgc	tggtctttct	gagtcacagc	tgcgaggtga	1800
tgggggctgg	ggccccaggc	gtcagcctcc	cagagggaca	gctgagcccc	1850
ctgccttggc	tccaggttgg	tagaagcagc	cgaagggcctc	ctgacagtgg	1900
ccagggaccc	ctgggtcccc	caggcctgca	gatgtttcta	tgaggggcag	1950
agctccttgg	tacatccatg	tgtggctctg	ctccaccctt	gtgccacccc	2000
agagccctgg	ggggtggtct	ccatgcctgc	caccctggca	tcggttttct	2050
gtgccgcctc	ccacacaaat	cagccccaga	aqgccccqgg	gccttqqctt	2100

Questions are asked about the following:

- (a) The number of people who have been convicted of a crime.
- (b) The number of people who have been sentenced to prison.
- (c) The number of people who have been released from prison.

<211> 281

<213> Homo Sapien

Met Gly Ser Arg Gly Gln Gly Leu Leu Leu Ala Tyr Cys Leu Leu
1 5 10 15

Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser
35 40 45

Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg
65 70 75

Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly
95 100 105

58

				110					115					120
Ala	Arg	Gly	His	Thr 125	Gly	Pro	Lys	Gly	Gln 130	Lys	Gly	Ser	Met	Gly 135
Ala	Pro	Gly	Glu	Arg 140	Cys	Lys	Ser	His	Tyr 145	Ala	Ala	Phe	Ser	Val 150
Gly	Arg	Lys	Lys	Pro 155	Met	His	Ser	Asn	His 160	Tyr	Tyr	Gln	Thr	Val 165
Ile	Phe	Asp	Thr	Glu 170	Phe	Val	Asn	Leu	Tyr 175	Asp	His	Phe	Asn	Met 180
Phe	Thr	Gly	Lys	Phe 185	Tyr	Cys	Tyr	Val	Pro 190	Gly	Leu	Tyr	Phe	Phe 195
Ser	Leu	Asn	Val	His 200	Thr	Trp	Asn	Gln	Lys 205	Glu	Thr	Tyr	Leu	His 210
Ile	Met	Lys	Asn	Glu 215	Glu	Glu	Val	Val	Ile 220	Leu	Phe	Ala	Gln	Val 225
Gly	Asp	Arg	Ser	Ile 230	Met	Gln	Ser	Gln	Ser 235	Leu	Met	Leu	Glu	Leu 240
Arg	Glu	Gln	Asp	Gln 245	Val	Trp	Val	Arg	Leu 250	Tyr	Lys	Gly	Glu	Arg 255
Glu	Asn	Ala	Ile	Phe 260	Ser	Glu	Glu	Leu	Asp 265	Thr	Tyr	Ile	Thr	Phe 270
Ser	Gly	Tyr	Leu	Val 275	Lys	His	Ala	Thr	Glu 280	Pro				

<210> 79

<212> DNA

<220>

<400> 79

<210> 80

<212> DNA

<220>

<400> 80

<210> 81

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
cccgtgctt gcgctgctgt gaccccggtta cctccatgta cccgg 45

<210> 82
<211> 2284
<212> DNA
<213> Homo Sapien

<400> 82
gcggagcatc cgctgcggtc ctgcgcgaga ccccgcgcg gattcgccgg 50
tcttccccgc gggcgcgaca gagctgtcct cgcacctgga tggcagcagg 100
ggcgccgggg tctctcgcac gccagagaga aatctcatca tctgtgcagc 150
cttcttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200
gacaaaaact aaactgaaat ttaaaatggt cttcggggga gaaggagct 250
tgacttacac tttggtaata atttgcttcc tgacactaag gctgtctgct 300
agtcagaatt gctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350
gtcatctctt tctaaggga tcaaggcaa tgagcccgta tatacttcaa 400
ctcaagaaga ctgcattaat tcttgctgtt caacaaaaaa catatcaggg 450
gacaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500
acceaaactgc tacctatctt tctgtcccaa cgaggaagcc tgtccattga 550
aaccagcaaa aggacttatg agttacagga taattacaga tttccatct 600
ttgaccagaa atttgccaag ccaagagtta cccaggaag attctctctt 650
acatggccaa ttttcacaag cagtcactcc cctagcccat catcacacag 700
attattcaaa gccaccgat atctcatgga gagacacact ttctcagaag 750
tttgatcct cagatcacct ggagaaacta ttaagatgg atgaagcaag 800
tgccagctc cttgcttata aggaaaaagg ccattctcag agttcacaat 850
tttctctga tcaagaaata gctcatctgc tgctgaaaa tgtgagtgcg 900
ctcccageta cggtggcagt tgettctcca cataccacct cggctactcc 950
aaagcccgcc acccttctac ccaccaatgc ttcagtgaca ccttctggga 1000
cttcccagcc acagctggcc accacagctc cacctgtaac cactgtcact 1050

[illegible]

<211> 431

<213> Home

Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile

1

5

10

15

00943780-00001

Ile Cys Phe Leu Thr	Leu Arg Leu Ser Ala	Ser Gln Asn Cys Leu
20	25	30
Lys Lys Ser Leu Glu Asp Val Val	Ile Asp Ile Gln Ser Ser Leu	
35	40	45
Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln		
50	55	60
Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly		
65	70	75
Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala		
80	85	90
Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala		
95	100	105
Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile		
110	115	120
Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu		
125	130	135
Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val		
140	145	150
Thr Pro Leu Ala His His His Thr Asp Tyr Ser Lys Pro Thr Asp		
155	160	165
Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp		
170	175	180
His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu		
185	190	195
Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln Phe Ser		
200	205	210
Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser Ala		
215	220	225
Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala		
230	235	240
Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr		
245	250	255
Pro Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro		
260	265	270
Val Thr Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr		
275	280	285
Val Phe Thr Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr		
290	295	300
Ala Val Leu Thr Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly		

305	310	315
Ser Leu Glu Thr Ile Pro Phe Thr Glu	Ile Ser Asn Leu Thr Leu	
320	325	330
Asn Thr Gly Asn Val Tyr Asn Pro Thr	Ala Leu Ser Met Ser Asn	
335	340	345
Val Glu Ser Ser Thr Met Asn Lys Thr	Ala Ser Trp Glu Gly Arg	
350	355	360
Glu Ala Ser Pro Gly Ser Ser Ser Gln	Gly Ser Val Pro Glu Asn	
365	370	375
Gln Tyr Gly Leu Pro Phe Glu Lys Trp	Leu Leu Ile Gly Ser Leu	
380	385	390
Leu Phe Gly Val Leu Phe Leu Val Ile	Gly Leu Val Leu Leu Gly	
395	400	405
Arg Ile Leu Ser Glu Ser Leu Arg Arg	Lys Arg Tyr Ser Arg Leu	
410	415	420
Asp Tyr Leu Ile Asn Gly Ile Tyr Val	Asp Ile	
425	430	

<210> 84
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 84
 agggaggatt atccttgacc tttgaagacc 30

 <210> 85
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 85
 gaagcaagtg cccagctc 18

 <210> 86
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 86
 cggtccctg ctctttgg 18

<210> 87
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
caccgtagct gggagcgcac tcac 24

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
agtgttaagtc aagctccc 18

<210> 89
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
gcttcctgac actaaggctg tctgctagtc agaattgcct caaaaagag 49

<210> 90
<211> 957
<212> DNA
<213> Homo Sapien

<400> 90
cctggaagat ggcgccattg gctgggtggcc tgctcaaggt ggtgttcgtg 50
gtcttcgcct ccttgtgtgc ctgggtattcg gggtagctgc tcgcagagct 100
cattccagat gcaccctgt ccagtgtgc ctatagcatc cgcagcatcg 150
gggagaggcc tgtcctcaaa gctccagtcc ccaaaaggca aaaatgtgac 200
caotggactc cctgcccata tgacacctat gcttacaggt tactcagcgg 250
agggtggcaga agcaagtacg ccaaaatctg ctttgaggat aacctactta 300
tgggagaaca gctgggaaat gttgccagag gaataaacat tgccattgtc 350
aactatgtaa ctgggaatgt gacagcaaca cgatgttttg atatgtatga 400
aggcgataac totggaccga tgacaaagtt tattcagagt gctgctccaa 450
aatccctgct cttcatggtg acctatgacg acggaagcac aagactgaat 500

aacgatgccca agaatgccat agaagcactt ggaagtaaag aaatcaggaa 550
 catgaaattc aggtctagct gggatattat tgcagcaaaa ggcttggaac 600
 tcccttccga aattcagaga gaaaagatca accactctga tgctaagaac 650
 aacagatatt ctggctggcc tgcagagatc cagatagaag gctgcatacc 700
 caaagaacga agctgacact gcagggtcct gagtaaagt gttctgtata 750
 aacaaatgca gctggaatcg ctcaagaatc ttatttttct aaatccaaca 800
 gcccatatth gatgagtatt ttgggtttgt tgtaaaccac tgaacatttg 850
 ctagtgtat caaatcttgg tacgcagtat ttttatacca gtattttatg 900
 tagtgaagat gtcaattagc aggaaactaa aatgaatgga aattcttaaa 950
 aaaaaaa 957

<210> 91
 <211> 235
 <212> PRT
 <213> Homo Sapien

<400> 91
 Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val
 1 5 10 15
 Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu
 20 25 30
 Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg
 35 40 45
 Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg
 50 55 60
 Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
 65 70 75
 Tyr Arg Leu Leu Ser Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile
 80 85 90
 Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val
 95 100 105
 Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn
 110 115 120
 Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser
 125 130 135
 Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu
 140 145 150
 Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn
 155 160 165

Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser Lys Glu Ile Arg
170 175 180

Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala Ala Lys Gly
185 190 195

Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn His Ser
200 205 210

Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile Gln
215 220 225

Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
230 235

<210> 92

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 92

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